

GenCore version: 4.5  
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## OM nucleic - nucleic search, using sw model.

Run on:

September 17, 2002, 00:04:09 ; Search time 3347.31 Seconds

(without alignments)

11588.820 Million cell updates/sec

Title: US-09-719-017a-2  
 Perfect score: 1793  
 Sequence: 1 gaattccctgttacaaat... caattactcaatggcccg 1793  
 Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0  
 Searched: 21979536 seqs, 10817449327 residues  
 Total number of hits satisfying chosen parameters: 43959072  
 Minimum DB seq length: 0  
 Maximum DB seq length: 200000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Pending\_Patents\_NA\_Main:  
 1: /cgn2\_6/ptodata/2/pna/PCRTUS\_COMBO.seq: \*  
 2: /cgn2\_6/ptodata/2/pna/US0506\_COMBO.seq: \*  
 3: /cgn2\_6/ptodata/2/pna/US077\_COMBO.seq: \*  
 4: /cgn2\_6/ptodata/2/pna/US080\_COMBO.seq: \*  
 5: /cgn2\_6/ptodata/2/pna/US081\_COMBO.seq: \*  
 6: /cgn2\_6/ptodata/2/pna/US082\_COMBO.seq: \*  
 7: /cgn2\_6/ptodata/2/pna/US083\_COMBO.seq: \*  
 8: /cgn2\_6/ptodata/2/pna/US084\_COMBO.seq: \*  
 9: /cgn2\_6/ptodata/2/pna/US085\_COMBO.seq: \*  
 10: /cgn2\_6/ptodata/2/pna/US087\_COMBO.seq: \*  
 11: /cgn2\_6/ptodata/2/pna/US088\_COMBO.seq: \*  
 12: /cgn2\_6/ptodata/2/pna/US089\_COMBO.seq: \*  
 13: /cgn2\_6/ptodata/2/pna/US090\_COMBO.seq: \*  
 14: /cgn2\_6/ptodata/2/pna/US091\_COMBO.seq: \*  
 15: /cgn2\_6/ptodata/2/pna/US092\_COMBO.seq: \*  
 16: /cgn2\_6/ptodata/2/pna/US093\_COMBO.seq: \*  
 17: /cgn2\_6/ptodata/2/pna/US094\_COMBO.seq: \*  
 18: /cgn2\_6/ptodata/2/pna/US095\_COMBO.seq: \*  
 19: /cgn2\_6/ptodata/2/pna/US095A\_COMBO.seq: \*  
 20: /cgn2\_6/ptodata/2/pna/US095B\_COMBO.seq: \*  
 21: /cgn2\_6/ptodata/2/pna/US095C\_COMBO.seq: \*  
 22: /cgn2\_6/ptodata/2/pna/US096\_COMBO.seq: \*  
 23: /cgn2\_6/ptodata/2/pna/US096A\_COMBO.seq: \*  
 24: /cgn2\_6/ptodata/2/pna/US096B\_COMBO.seq: \*  
 25: /cgn2\_6/ptodata/2/pna/US096C\_COMBO.seq: \*  
 26: /cgn2\_6/ptodata/2/pna/US096D\_COMBO.seq: \*  
 27: /cgn2\_6/ptodata/2/pna/US096E\_COMBO.seq: \*  
 28: /cgn2\_6/ptodata/2/pna/US099A\_COMBO.seq: \*  
 29: /cgn2\_6/ptodata/2/pna/US099B\_COMBO.seq: \*  
 30: /cgn2\_6/ptodata/2/pna/US099C\_COMBO.seq: \*  
 31: /cgn2\_6/ptodata/2/pna/US099D\_COMBO.seq: \*  
 32: /cgn2\_6/ptodata/2/pna/US099E\_COMBO.seq: \*  
 33: /cgn2\_6/ptodata/2/pna/US099F\_COMBO.seq: \*  
 34: /cgn2\_6/ptodata/2/pna/US099G\_COMBO.seq: \*  
 35: /cgn2\_6/ptodata/2/pna/US099H\_COMBO.seq: \*  
 36: /cgn2\_6/ptodata/2/pna/US099I\_COMBO.seq: \*  
 37: /cgn2\_6/ptodata/2/pna/US100\_COMBO.seq: \*  
 38: /cgn2\_6/ptodata/2/pna/US101\_COMBO.seq: \*  
 39: /cgn2\_6/ptodata/2/pna/US6000\_COMBO.seq: \*  
 40: /cgn2\_6/ptodata/2/pna/US6001\_COMBO.seq: \*  
 41: /cgn2\_6/ptodata/2/pna/US6002\_COMBO.seq: \*  
 42: /cgn2\_6/ptodata/2/pna/US6003\_COMBO.seq: \*  
 43: /cgn2\_6/ptodata/2/pna/US6004\_COMBO.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	954.2	53.2	1071	31 US-09-806-876A-1 Sequence 1, Appli
2	401.6	22.4	7615	15 US-09-108-01-87 Sequence 87, Appli
3	401.6	22.4	7615	19 US-09-502-42-87 Sequence 87, Appli
4	401.6	22.4	7615	19 US-09-502-49-87 Sequence 87, Appli
5	401.6	22.4	7688	15 US-09-108-01-89 Sequence 89, Appli
6	401.6	22.4	7688	19 US-09-502-42-89 Sequence 89, Appli
7	401.6	22.4	7688	19 US-09-502-49-89 Sequence 89, Appli
8	401.6	22.4	7797	15 US-09-108-01-88 Sequence 88, Appli
9	401.6	22.4	7797	19 US-09-502-42-88 Sequence 88, Appli
10	401.6	22.4	7797	19 US-09-502-49-88 Sequence 88, Appli
11	369	20.6	7416	34 US-09-900-57-46 Sequence 46, Appli
12	369	18.7	5641	24 US-09-630-931A-13 Sequence 13, Appli
13	336	18.7	5670	24 US-09-630-931A-14 Sequence 14, Appli
14	336	18.7	5626	24 US-09-630-931A-11 Sequence 11, Appli
15	336	18.7	6043	24 US-09-630-929-4 Sequence 4, Appli
16	336	18.7	6071	24 US-09-630-931A-12 Sequence 12, Appli
17	332.8	18.6	4214	33 US-09-869-696-1 Sequence 1, Appli
18	332.8	18.6	4214	30 US-09-795-872-10 Sequence 10, Appli
19	332.8	18.6	5013	15 US-09-183-188A-5 Sequence 5, Appli
20	332.8	18.6	5013	15 US-09-183-188B-5 Sequence 5, Appli
21	332.8	18.6	5027	1 PCP-US98-27498-6 Sequence 6, Appli
22	332.8	18.6	5027	1 PCP-US98-27498-12 Sequence 12, Appli
23	332.8	18.6	5069	1 PCP-US98-27498-15 Sequence 15, Appli
24	332.8	18.6	5069	1 PCP-US98-27498-15 Sequence 12, Appli
25	332.8	18.6	5069	13 US-08-996-744-12 Sequence 15, Appli
26	332.8	18.6	5069	13 US-08-996-744-15 Sequence 15, Appli
27	332.8	18.6	5099	1 PCP-US98-27498-6 Sequence 6, Appli
28	332.8	18.6	5132	1 PCP-US98-27498-24 Sequence 24, Appli
29	332.8	18.6	5132	13 US-08-996-744-24 Sequence 24, Appli
30	332.8	18.6	5324	1 PCP-US98-27498-31 Sequence 31, Appli
31	332.8	18.6	5324	13 US-08-996-744-31 Sequence 31, Appli











FILE REFERENCE: ELITRA.006A  
 CURRENT APPLICATION NUMBER: US/09/630,931A  
 PRIORITY FILING DATE: 2000-08-02  
 PRIORITY APPLICATION NUMBER: 60/159,221  
 NUMBER OF SEQ ID NOS: 19  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 13  
 LENGTH: 5841  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: PDJM3  
 US-09-630-931A-13

Query Match 18.7%; Score 336; DB 24; Length 5641;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-80; Mismatches 0;  
 Matches 336; Conservative 0; Indels 0; Gaps 0;

QY 1311 atgcgcgaactcagaactaaacccgttagctgggtctccccatcg 1500  
 QY 1371 agatgttggaaactgcaggcatcaataaacaaacaaaggctcagtggaaactggcct 1430  
 Db 1501 aggttaggaactgcaggcatcaataaacaaacaaaggctcagtggaaactggcct 1560  
 Db 1441 atgcgcgaactcagaactggaaacacgcgcgttaggcgcgtatgtgggttcctccatcg 1500  
 QY 1311 atgcgcgaactcagaactggaaacacgcgcgttaggcgcgtatgtgggttcctccatcg 1370  
 QY 1491 ggattttgcgttgtttgtcggtttgtcggtttgtggatggacaaatccgcggcggc 1490  
 Db 1561 tcgttttatctgttgtttgtcggtttgtcggtttgtggatggacaaatccgcggcggc 1620  
 QY 1491 ggattttgcgttgtttgtcggtttgtcggtttgtggatggacaaatccgcggcggc 1550  
 Db 1561 tcgttttatctgttgtttgtcggtttgtcggtttgtggatggacaaatccgcggcggc 1680  
 QY 1551 tgccaggcatcaattaaaggagaagccatccatcgcgtggcccttttgcgttctaca 1610  
 Db 1621 ggattttgcgttgtttgtcggtttgtcggtttgtggatggacaaatccgcggcggc 1740  
 QY 1681 tgccaggcatcaattaaaggagaagccatccatcgcgtggcccttttgcgttctaca 1646  
 Db 1741 aactcttcctgtcgcatatctacacgcctccccc 1776

RESULT 14  
 US-09-630-931A-11  
 Sequence 11, Application US/09630931A  
 GENERAL INFORMATION:  
 APPLICANT: ZYSKIND, Judith W.  
 FILE REFERENCE: CHITROBIASE AS A REPORTER ENZYME  
 CURRENT APPLICATION NUMBER: US/09/630,931A  
 CURRENT FILING DATE: 2000-08-02  
 PRIORITY FILING DATE: 1999-10-13  
 NUMBER OF SEQ ID NOS: 19  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 11  
 LENGTH: 5826  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: PDYK9  
 US-09-630-931A-11

Query Match 18.7%; Score 336; DB 24; Length 5826;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-80; Mismatches 0;  
 Matches 336; Conservative 0; Indels 0; Gaps 0;

QY 1311 atgcgcgaactcagaactaaacccgttagctgggtctccccatcg 1370  
 Db 1441 atgcgcgaactcagaactggaaacacgcgcgttaggcgcgtatgtgggttcctccatcg 1500  
 QY 1371 agatgttggaaactgcaggcatcaataaacaaacaaaggctcagtggaaactggcct 1430  
 Db 1501 agatgttggaaactgcaggcatcaataaacaaacaaaggctcagtggaaactggcct 1560  
 QY 1431 tcgttttatctgttgtttgtcggtttgtcggtttgtggatggacaaatccgcggcggc 1490  
 Db 1561 tcgttttatctgttgtttgtcggtttgtcggtttgtggatggacaaatccgcggcggc 1620  
 QY 1491 ggattttgcgttgtttgtcggtttgtcggtttgtggatggacaaatccgcggcggc 1550  
 Db 1621 ggattttgcgttgtttgtcggtttgtcggtttgtggatggacaaatccgcggcggc 1680  
 QY 1551 tgccaggcatcaattaaaggagaagccatccatcgcgtggcccttttgcgttctaca 1610  
 Db 1681 tgccaggcatcaattaaaggagaagccatccatcgcgtggcccttttgcgttctaca 1740  
 QY 1611 aactcttcctgtcgcatatctacacgcctccccc 1776

RESULT 15  
US-09-630-929-4  
Sequence 4 Application US/09630929  
GENERAL INFORMATION:  
APPLICANT: Judith W. Zyskind  
TITLE OF INVENTION: USE OF ECOTOENZYMES AND SECRETED ENZYMES  
TITLE OF INVENTION: TO MONITOR CELLULAR PROLIFERATION  
FILE REFERENCE: ELITRA\_012A  
CURRENT APPLICATION NUMBER: US-09-630,929  
CURRENT FILING DATE: 2000-08-02  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 6043  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Engineered E. coli plasmid pJFK4 with V. harveyi  
OTHER INFORMATION: sequences inserted  
US-09-630-929-4

Query Match	18.7%	Score	336	DB	24	Length	6043	
Best Local Similarity	100.0%	Pred.	No.	1	8e-80			
Matches	336	Conservative	0	Mismatches	0	Indels	0	gaps
Qy	1311	atgcgcgaactcagaagtgaaacggccgttagcgccgatgttagtggggctcccccattcg	9	1370				
Dy	1441	atgcgcgaactcagaagtgaaacggccgttagcgccgatgttagtggggctcccccattcg	9	1500				
Qy	1371	agagtgggaactggccggcaccaataaaaaaaaaggaaaggctcatcgaaagactggcc	t	1430				
Dy	1501	agagtaggaaactggccggcaccaataaacgaaaggctcagtcagtcgaaagactggcc	t	1560				
Oy	1431	tgtttttatcttttgtgtcgctgtggtaggacaatccggggac	c	1490				
Dy	1561	tgtttttatcttttgtgtcgctgtggtaggacaatccggggac	c	1620				
Oy	1491	ggatttggaaacctgtggaaacggccggagggtggggcggacccgcataac	c	1550				
Dy	1621	ggatttggaaacctgtggaaacggccggagggtggggcggacccgcataac	c	1680				
Oy	1551	tgccaaagcatcaaatatragataaaggccatcttgacgatggccttttgcgttctaca	a	1610				
Dy	1681	tgccaaagcatcaaatatragataaaggccatcttgacgatggccttttgcgttctaca	a	1740				
Oy	1611	aactcttcctgtcgcttatctacaaaggccatcccc	t	1646				
Dy	1741	aactcttcctgtcgcttatctacaaaggccatcccc	t	1776				

Search completed: September 17, 2002, 02:38:37  
Job time: 9268 sec